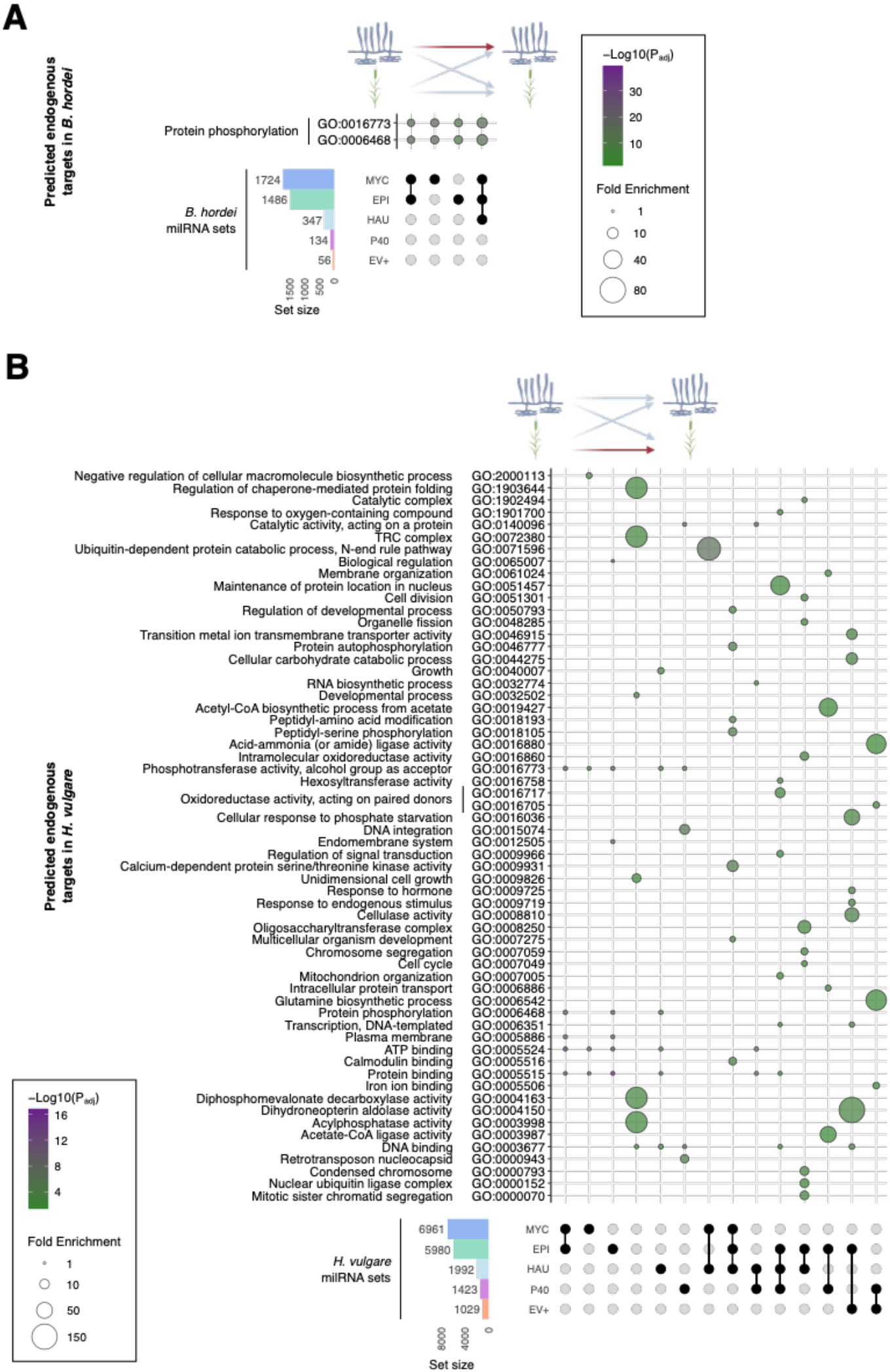
A
Predicted endogenous targets in B. hordei
Protein phosphorylation
GO:0016773
GO:0006468
B. hordei milRNA sets
1724
1486
347
134
56
MYC
EPI
HAU
P40
EV+
1500
1000
500
0
Set size
−Log10(Padj)
30
20
10
Fold Enrichment
1
10
40
80
B
Predicted endogenous targets in H. vulgare
Negative regulation of cellular macromolecule biosynthetic process GO:2000113
Regulation of chaperone-mediated protein folding GO:1903644
Catalytic complex GO:1902494
Response to oxygen-containing compound GO:1901700
Catalytic activity, acting on a protein GO:0140096
TRC complex GO:0072380
Ubiquitin-dependent protein catabolic process, N-end rule pathway GO:0071596
Biological regulation GO:0065007
Membrane organization GO:0061024
Maintenance of protein location in nucleus GO:0051457
Cell division GO:0051301
Regulation of developmental process GO:0050793
Organelle fission GO:0048285
Transition metal ion transmembrane transporter activity GO:0046915
Protein autophosphorylation GO:0046777
Cellular carbohydrate catabolic process GO:0044275
Growth GO:0040007
RNA biosynthetic process GO:0032774
Developmental process GO:0032502
Acetyl-CoA biosynthetic process from acetate GO:0019427
Peptidyl-amino acid modification GO:0018193
Peptidyl-serine phosphorylation GO:0018105
Acid-ammonia (or amide) ligase activity GO:0016880
Intramolecular oxidoreductase activity GO:0016860
Phosphotransferase activity, alcohol group as acceptor GO:0016773
Hexosyltransferase activity GO:0016758
Oxidoreductase activity, acting on paired donors GO:0016717
GO:0016705
Cellular response to phosphate starvation GO:0016036
DNA integration GO:0015074
Endomembrane system GO:0012505
Regulation of signal transduction GO:0009966
Calcium-dependent protein serine/threonine kinase activity GO:0009931
Unidimensional cell growth GO:0009826
Response to hormone GO:0009725
Response to endogenous stimulus GO:0009719
Cellulase activity GO:0008810
Oligosaccharyltransferase complex GO:0008250
Multicellular organism development GO:0007275
Chromosome segregation GO:0007059
Cell cycle GO:0007049
Mitochondrion organization GO:0007005
Intracellular protein transport GO:0006886
Glutamine biosynthetic process GO:0006542
Protein phosphorylation GO:0006468
Transcription, DNA-templated GO:0006351
Plasma membrane GO:0005886
ATP binding GO:0005524
Calmodulin binding GO:0005516
Protein binding GO:0005515
Iron ion binding GO:0005506
Diphosphomevalonate decarboxylase activity GO:0004163
Dihydroneopterin aldolase activity GO:0004150
Acylphosphatase activity GO:0003998
Acetate-CoA ligase activity GO:0003987
DNA binding GO:0003677
Retrotransposon nucleocapsid GO:0000943
Condensed chromosome GO:0000793
Nuclear ubiquitin ligase complex GO:0000152
Mitotic sister chromatid segregation GO:0000070
H. vulgare milRNA sets
6961
5980
1992
1423
1029
MYC
EPI
HAU
P40
EV+
8000
4000
0
Set size
−Log10(Padj)
16
12
8
4
Fold Enrichment
1
10
50
150

Supplementary Figure 12. GO enrichment of putative endogenous milRNA targets. We determined all putative targets of the sets of *B. hordei* and *H. vulgare* milRNAs via psRNAtarget (Dai and Zhao 2011). We used ShinyGO v0.75 (Ge *et al.* 2020) to calculate enriched gene ontology (GO) terms in all milRNA target sets and summarized redundant GO terms with EMBL-EBI QuickGO (https://www.ebi.ac.uk/QuickGO/) on GO version 2022-04-26 and REVIGO (Supek *et al.* 2011). (**A**) GO enrichment terms found in putative endogenous targets of *B. hordei* milRNAs. (**B**) GO enrichment terms found in putative endogenous targets of *H. vulgare* milRNAs. The GO terms and identifiers are indicated next to the bubble plots. Bubble size indicates fold enrichment of the term in the respective subset, fill color indicates -Log10 of the FDR-adjusted enrichment *P* value. The milRNA subsets are indicated below the bubble plots (see Figure 4 for all subsets). The icons on top of the plot were created with bioRender.com; the blue mycelium indicates *B. hordei* and the green plant barley.